

109672

Schreiber, David

From: Steadman, David (AU1652)
Sent: Thursday, November 13, 2003 9:51 AM
To: Schreiber, David
Subject: 09/508,418 sequence search request

NAME: David Steadman
AU: 1652
Date: 11/13/03
Office: 10D-04
Mailbox: 10D-01

Mr. Schreiber, please search the following sequences in commercial and interference databases:

- 1) Standard search of SEQ ID NO:2 against amino acid databases.
- 2) Standard search of SEQ ID NO:2 against nucleic acid databases.

Please save results to diskette.

Thank you very much.

David J. Steadman
Patent Examiner
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T04058

C:Species: *Nicotiana tabacum* (common tobacco)

~~C;Accession:~~ T04058

Proc. Natl. Acad. Sci. U.S.A. 94, 8895-8900, 1997

A;Reference number: Z15186; MUID:97385200; PMID:9238074

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-548 <LER>

A; Experimental source: strain SR1

A; Gene: ppxI

A;Pathway: tetrapyrrole synthesis

F;1-50/Domain: transit peptide (chloroplast) #status predicted <TNP>

F;51-548/Product: protoporphyrinogen oxidase IX #status predicted <MAT>

Query Match 99.2%; Score 2821; DB 2; Length 548;
Best Local Similarity 99.3%; Pred. No. 4.3e-200;
Matches 544; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MTTTPIANHPNIFTHQSSSSPLAFLNRTSFIPFSSISKRNSVNCNGWRTRCSVAKDYTV	60
Db	1	MTTTPIANHPNIFTHQSSSSPLAFLNRTSFIPFSSISKRNSVNCNGWRTRCSVAKDYTV	60
Qy	61	SSAVDGGPAAELDCVIVGAGISGLCIAQVMSANYPNLMVTEARDRAGGNITTVERDGYLW	120
Db	61	SSAVDGGPAAELDCVIVGAGISGLCIAQVMSANYPNLMVTEARDRAGGNITTVERDGYLW	120
Qy	121	EEGPNSFQPSDPMLTMAVDCGLKDDLVLGDPNAPRFVLWKGKLRPVPSKLTDLPPFFDLMS	180
Db	121	EEGPNSFQPSDPMLTMAVDCGLKDDLVLGDPNAPRFVLWKGKLRPVPSKLTDLAFFDLMS	180
Qy	181	IPGKLRAFGPIGLRSPPGHEESVEQFVRRNLGGEVFERLIEPFCSGVYVGDP SKLSMK	240
Db	181	IPGKLRAFGAIGLRSPPGHEESVEQFVRRNLGGEVFERLIEPFCSGVYAGDP SKLSMK	240
Qy	241	AAF GK V W K L E E T G G S I I G G T F K A I K E R S S T P K A P R D P R L P K P K G Q T V G S F R K G L R M L P D A	300
Db	241	AAF GK V W K L E E T G G S I I G G T F K A I K E R S S T P K A P R D P R L P K P K G Q T V G S F R K G L R M L P D A	300
Qy	301	I S A R L G S K L K L S W K L S S I T K S E K G G Y H L T Y E T P E G V V S L Q S R S I V M T V P S Y V A S N I L R P L	360
Db	301	I S A R L G S K L K L S W K L S S I T K S E K G G Y H L T Y E T P E G V V S L Q S R S I V M T V P S Y V A S N I L R P L	360
Qy	361	S V A A A D A L S N F Y Y P P V G A V T I S Y P Q E A I R D E R L V D G E L K G F G Q L H P R T Q G V E T L G T I Y S S	420
Db	361	S V A A A D A L S N F Y Y P P V G A V T I T Y P O E A I R D E R L V D G E L K G F G Q L H P R T O G V E T L G T I Y S S	420

[illegible]